RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/622,869*
Source: *FWO*
Date Processed by STIC: *1/4/04*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: *10/622,869* |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

1,2 -12 (maybe more)

5____ Variable Length — Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

RAW SEQUENCE LISTING   DATE: 01/04/2004
PATENT APPLICATION: **US/10/622,869**   TIME: 14:04:41

Input Set : **A:\29310-20036.00.TXT**
Output Set: **N:\CRF4\01022004\J622869.raw**

```
 4 <110> APPLICANT: TIKOO, Suresh K.
 6 <120> TITLE OF INVENTION: PAV REGIONS FOR ENCAPSIDATION AND E1
 7          TRANSCRIPTIONAL CONTROL
 9 <130> FILE REFERENCE: .293102003600
11 <140> CURRENT APPLICATION NUMBER: US 10/622,869
12 <141> CURRENT FILING DATE: 2003-07-18
14 <150> PRIOR APPLICATION NUMBER: US 60/397,251
15 <151> PRIOR FILING DATE: 2002-07-19
17 <150> PRIOR APPLICATION NUMBER: US 60/460,798
18 <151> PRIOR FILING DATE: 2003-04-04
20 <160> NUMBER OF SEQ ID NOS: 114
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 7
26 <212> TYPE: DNA
27 <213> ORGANISM: Porcine Adenovirus
29 <220> FEATURE:
30 <221> NAME/KEY: misc_feature
31 <222> LOCATION: 1
32 <223> OTHER INFORMATION: n=g or gg or cgg or gcgg or ggcgg
34 <220> FEATURE:
35 <221> NAME/KEY: misc_feature
36 <222> LOCATION: 7
37 <223> OTHER INFORMATION: n=cccgcaca or cccgcac or cccgca or cccgc or cccg
38      or ccc or cc or c
40 <220> FEATURE:
41 <221> NAME/KEY: misc_feature
42 <222> LOCATION: 1, 7
43 <223> OTHER INFORMATION: n = A,T,C or G
45 <400> SEQUENCE: 1
46 naaattn                                                            7
48 <210> SEQ ID NO: 2
49 <211> LENGTH: 7
50 <212> TYPE: DNA
51 <213> ORGANISM: Porcine Adenovirus
53 <220> FEATURE:
54 <221> NAME/KEY: misc_feature
55 <222> LOCATION: 1
56 <223> OTHER INFORMATION: n=g or gg or ggg or cggg or gcggg
58 <220> FEATURE:
59 <221> NAME/KEY: misc_feature
60 <222> LOCATION: 7
61 <223> OTHER INFORMATION: n=gtgccctct or gtgccctc or gtgccct or gtgccc or
```

W-->

handwritten annotations:
pp 1-6
Does Not Comply
Corrected Diskette Needed

variable length is not permitted - "n" can only represent a single nucleotide (see item 5 on Error Summary Sheet)

variable length not permitted

```
     62      gtgcc or gtgc or gtg or gt or g
     64 <220> FEATURE:
     65 <221> NAME/KEY: misc_feature
     66 <222> LOCATION: 1, 7
     67 <223> OTHER INFORMATION: n = A,T,C or G
     69 <400> SEQUENCE: 2
W--> 70 nattttn                                              7
     72 <210> SEQ ID NO: 3
     73 <211> LENGTH: 6
     74 <212> TYPE: DNA
     75 <213> ORGANISM: Porcine Adenovirus
     77 <220> FEATURE:                       same error
     78 <221> NAME/KEY: misc_feature
     79 <222> LOCATION: 1
     80 <223> OTHER INFORMATION: n=g or gg or cgg or ccgg or cccgg
     82 <220> FEATURE:
     83 <221> NAME/KEY: misc_feature
     84 <222> LOCATION: 6
     85 <223> OTHER INFORMATION: n=ccccacctg or ccccacct or ccccacc or ccccac or
     86      cccca or cccc or ccc or cc or c
     88 <220> FEATURE:
     89 <221> NAME/KEY: misc_feature
     90 <222> LOCATION: 1, 6
     91 <223> OTHER INFORMATION: n = A,T,C or G
     93 <400> SEQUENCE: 3
W--> 94 ntattn                                               6
     96 <210> SEQ ID NO: 4
     97 <211> LENGTH: 10
     98 <212> TYPE: DNA
     99 <213> ORGANISM: Porcine Adenovirus
    101 <220> FEATURE:
    102 <221> NAME/KEY: misc_feature
    103 <222> LOCATION: 1                    same error
    104 <223> OTHER INFORMATION: n=g or tg or gtg or ggtg or gggtg
    106 <220> FEATURE:
    107 <221> NAME/KEY: misc_feature
    108 <222> LOCATION: 10
    109 <223> OTHER INFORMATION: n=cccctca or cccctc or cccct or cccc or ccc or cc
    110      or c
    112 <220> FEATURE:
    113 <221> NAME/KEY: misc_feature
    114 <222> LOCATION: 1, 10
    115 <223> OTHER INFORMATION: n = A,T,C or G
    117 <400> SEQUENCE: 4
W--> 118 ntatttttn                                          10
    120 <210> SEQ ID NO: 5
    121 <211> LENGTH: 8
    122 <212> TYPE: DNA
    123 <213> ORGANISM: Porcine Adenovirus
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RAW SEQUENCE LISTING   DATE: 01/04/2004
PATENT APPLICATION: US/10/622,869   TIME: 14:04:41

Input Set : A:\29310-20036.00.TXT
Output Set: N:\CRF4\01022004\J622869.raw

```
125 <220> FEATURE:
126 <221> NAME/KEY: misc_feature
127 <222> LOCATION: 1
128 <223> OTHER INFORMATION: n=g or tg or gtg or agtg or cagtg
130 <220> FEATURE:
131 <221> NAME/KEY: misc_feature
132 <222> LOCATION: 8
133 <223> OTHER INFORMATION: n=gtccgcgc or gtccgcg or gtccgc or gtccg or gtcc
134       or gtc or gt or g
136 <220> FEATURE:
137 <221> NAME/KEY: misc_feature
138 <222> LOCATION: 1, 8
139 <223> OTHER INFORMATION: n = A,T,C or G
141 <400> SEQUENCE: 5
142 ntatatan                                                    8
144 <210> SEQ ID NO: 6
145 <211> LENGTH: 6
146 <212> TYPE: DNA
147 <213> ORGANISM: Porcine Adenovirus
149 <220> FEATURE:
150 <221> NAME/KEY: misc_feature
151 <222> LOCATION: 1
152 <223> OTHER INFORMATION: n=g or ag or gag or agag or tagag
154 <220> FEATURE:
155 <221> NAME/KEY: misc_feature
156 <222> LOCATION: 6
157 <223> OTHER INFORMATION: n=ctctcagcg or ctctcagc or ctctcag or ctctca or
158       ctctc or ctct or ctc or ct or c
160 <220> FEATURE:
161 <221> NAME/KEY: misc_feature
162 <222> LOCATION: 1, 6
163 <223> OTHER INFORMATION: n = A,T,C or G
165 <400> SEQUENCE: 6
166 ntttn                                                       6
168 <210> SEQ ID NO: 7
169 <211> LENGTH: 8
170 <212> TYPE: DNA
171 <213> ORGANISM: Porcine Adenovirus
173 <220> FEATURE:
174 <221> NAME/KEY: misc_feature
175 <222> LOCATION: 1
176 <223> OTHER INFORMATION: n=g or gg or tgg or ctgg
178 <220> FEATURE:
179 <221> NAME/KEY: misc_feature
180 <222> LOCATION: 8
181 <223> OTHER INFORMATION: n=c or cc or cca or ccac
183 <220> FEATURE:
184 <221> NAME/KEY: misc_feature
185 <222> LOCATION: 1, 8
```

W--> 142 (handwritten annotations: "same error", "same", "same")
W--> 166

```
   186 <223> OTHER INFORMATION: n = A,T,C or G
   188 <400> SEQUENCE: 7
W--> 189 ntattttn                                          8
   191 <210> SEQ ID NO: 8
   192 <211> LENGTH: 7
   193 <212> TYPE: DNA
   194 <213> ORGANISM: Porcine Adenovirus
   196 <220> FEATURE:
   197 <221> NAME/KEY: misc_feature
   198 <222> LOCATION: 1
   199 <223> OTHER INFORMATION: n=g or tg or gtg          same
   201 <220> FEATURE:
   202 <221> NAME/KEY: misc_feature
   203 <222> LOCATION: 7
   204 <223> OTHER INFORMATION: n=g or gg
   206 <220> FEATURE:
   207 <221> NAME/KEY: misc_feature
   208 <222> LOCATION: 1, 7
   209 <223> OTHER INFORMATION: n = A,T,C or G
   211 <400> SEQUENCE: 8
W--> 212 natattn                                           7
   214 <210> SEQ ID NO: 9
   215 <211> LENGTH: 6
   216 <212> TYPE: DNA
   217 <213> ORGANISM: Porcine Adenovirus
   219 <220> FEATURE:
   220 <221> NAME/KEY: misc_feature
   221 <222> LOCATION: 1
   222 <223> OTHER INFORMATION: n=c or cc                 same
   224 <220> FEATURE:
   225 <221> NAME/KEY: misc_feature
   226 <222> LOCATION: 6
   227 <223> OTHER INFORMATION: n=c or cc or cct or cctg or cctgg or cctggg
   229 <220> FEATURE:
   230 <221> NAME/KEY: misc_feature
   231 <222> LOCATION: 1, 6
   232 <223> OTHER INFORMATION: n = A,T,C or G
   234 <400> SEQUENCE: 9
W--> 235 ntttan                                            6
   237 <210> SEQ ID NO: 10
   238 <211> LENGTH: 9
   239 <212> TYPE: DNA
   240 <213> ORGANISM: Porcine Adenovirus
   242 <220> FEATURE:
   243 <221> NAME/KEY: misc_feature
   244 <222> LOCATION: 1
   245 <223> OTHER INFORMATION: n=c or tc or ctc          same.
   247 <220> FEATURE:
   248 <221> NAME/KEY: misc_feature
```

RAW SEQUENCE LISTING   DATE: 01/04/2004
PATENT APPLICATION: US/10/622,869   TIME: 14:04:41

Input Set : A:\29310-20036.00.TXT
Output Set: N:\CRF4\01022004\J622869.raw

```
      249 <222> LOCATION: 9
      250 <223> OTHER INFORMATION: n=c or cc or cca or ccac         same
      252 <220> FEATURE:
      253 <221> NAME/KEY: misc_feature
      254 <222> LOCATION: 1, 9
      255 <223> OTHER INFORMATION: n = A,T,C or G
      257 <400> SEQUENCE: 10
W--> 258 naattttan                                                  9
      260 <210> SEQ ID NO: 11
      261 <211> LENGTH: 8
      262 <212> TYPE: DNA
      263 <213> ORGANISM: Porcine Adenovirus
      265 <220> FEATURE:                          same
      266 <221> NAME/KEY: misc_feature
      267 <222> LOCATION: 1
      268 <223> OTHER INFORMATION: n=g or cg or tcg or gtcg or ggtcg
      270 <220> FEATURE:
      271 <221> NAME/KEY: misc_feature
      272 <222> LOCATION: 8
      273 <223> OTHER INFORMATION: n=c or cc or cca or ccac
      275 <220> FEATURE:
      276 <221> NAME/KEY: misc_feature
      277 <222> LOCATION: 1, 8
      278 <223> OTHER INFORMATION: n = A,T,C or G
      280 <400> SEQUENCE: 11
W--> 281 nattttn                                                    8
      283 <210> SEQ ID NO: 12
      284 <211> LENGTH: 10
      285 <212> TYPE: DNA
      286 <213> ORGANISM: Porcine Adenovirus
      288 <220> FEATURE:
      289 <221> NAME/KEY: misc_feature
      290 <222> LOCATION: 1
      291 <223> OTHER INFORMATION: n=c or cc or ccc
      293 <220> FEATURE:
      294 <221> NAME/KEY: misc_feature
      295 <222> LOCATION: 10
      296 <223> OTHER INFORMATION: n=c or ct or ctg or ctgc or ctgcg or ctgcgc or
      297       ctgcgcg
      299 <220> FEATURE:
      300 <221> NAME/KEY: misc_feature
      301 <222> LOCATION: 1, 10
      302 <223> OTHER INFORMATION: n = A,T,C or G
      304 <400> SEQUENCE: 12
W--> 305 ntatttattn                                                 10
      307 <210> SEQ ID NO: 13
      308 <211> LENGTH: 16
      309 <212> TYPE: DNA
      310 <213> ORGANISM: Porcine Adenovirus 3
```

Please correct this error in subsequent sequences

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/04/2004
PATENT APPLICATION: US/10/622,869   TIME: 14:04:42

Input Set : A:\29310-20036.00.TXT
Output Set: N:\CRF4\01022004\J622869.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1,7
Seq#:2; N Pos. 1,7
Seq#:3; N Pos. 1,6
Seq#:4; N Pos. 1,10
Seq#:5; N Pos. 1,8
Seq#:6; N Pos. 1,6
Seq#:7; N Pos. 1,8
Seq#:8; N Pos. 1,7
Seq#:9; N Pos. 1,6
Seq#:10; N Pos. 1,9
Seq#:11; N Pos. 1,8
Seq#:12; N Pos. 1,10
Seq#:31; N Pos. 5,6,7,8,9,10,11,12

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/622,869

DATE: 01/04/2004
TIME: 14:04:42

Input Set : A:\29310-20036.00.TXT
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```
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:70 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:118 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
```